

SEQUENCE LISTING

<110> Helix Research Institute

<120> NOVEL GENES ASSOCIATED WITH THE MAINTENANCE
OF DIFFERENTIATION OF SMOOTH MUSCLE CELLS

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<150> JP 1999-248036

<151> 1999-07-29

<150> JP 2000-118776

<151> 2000-01-11

<150> JP 2000-183767

<151> 2000-05-02

<150> US 60/159590

<151> 1999-10-18

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<151> 2000-02-17

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<170> PatentIn Ver. 2.0

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<213> Homo sapiens

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agcc atg gca gcg ctg cgc tac gcg ggg ctg gac gac acg gac agt gag 169

Met Ala Ala Leu Arg Tyr Ala Gly Leu Asp Asp Thr Asp Ser Glu

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gac gag ctg cct ccg ggc tgg gag gag aga acc acc aag gac ggc tgg 217

Asp Glu Leu Pro Pro Gly Trp Glu Glu Arg Thr Thr Lys Asp Gly Trp

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gtt tac tac gcc aat cac acc gag gag aag act cag tgg gaa cat cca 265

Val Tyr Tyr Ala Asn His Thr Glu Glu Lys Thr Gln Trp Glu His Pro

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aaa act gga aaa aga aaa cga gtg gca gga gat ttg cca tac gga tgg 313

Lys Thr Gly Lys Arg Lys Arg Val Ala Gly Asp Leu Pro Tyr Gly Trp

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gaa caa gaa act gat gag aac gga caa gtg ttt ttt gtt gac cat ata 361

Glu Gln Glu Thr Asp Glu Asn Gly Gln Val Phe Phe Val Asp His Ile

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aat aaa aga acc acc tac ttg gac cca aga ctg gcg ttt act gtg gat 409

Asn Lys Arg Thr Thr Tyr Leu Asp Pro Arg Leu Ala Phe Thr Val Asp

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gat aat ccg acc aag cca acc acc cgg caa aga tac gac ggc agc acc 457

Asp Asn Pro Thr Lys Pro Thr Thr Arg Gln Arg Tyr Asp Gly Ser Thr

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act gcc atg gaa att ctc cag ggc ccg gat ttc act ggc aaa gtg gtt 505

Thr Ala Met Glu Ile Leu Gln Gly Pro Asp Phe Thr Gly Lys Val Val

115

120

125

gtg gtc act gga gct aat tca gga ata ggg ttc gaa acc gcc aag tct 553

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 Val Gln Leu Leu Gln Asp Val Leu Cys Arg Ser Ala Pro Ala Arg Val
 240 245 250 255

att gtg gtc tcc tca gag tcc cat cga ttt aca gat att aac gac tcc 937
 Ile Val Val Ser Ser Glu Ser His Arg Phe Thr Asp Ile Asn Asp Ser
 260 265 270

ttg gga aaa ctg gac ttc agt cgc ctc tct cca aca aaa aac gac tat 985
 Leu Gly Lys Leu Asp Phe Ser Arg Leu Ser Pro Thr Lys Asn Asp Tyr
 275 280 285

tgg gcg atg ctg gct tat aac agg tcc aag ctc tgc aac atc ctc ttc 1033
 Trp Ala Met Leu Ala Tyr Asn Arg Ser Lys Leu Cys Asn Ile Leu Phe
 290 295 300

tcc aac gag ctg cac cgt cgc ctc tcc cca cgc ggg gtc acg tcg aac 1081
 Ser Asn Glu Leu His Arg Arg Leu Ser Pro Arg Gly Val Thr Ser Asn
 305 310 315

gca gtg cat cct gga aat atg atg tac tcc aac att cat cgc agc tgg 1129
 Ala Val His Pro Gly Asn Met Met Tyr Ser Asn Ile His Arg Ser Trp
 320 325 330 335

tgg gtg tac aca ctg ctg ttt acc ttg gcg agg cct ttc acc aag tcc 1177

Trp Val Tyr Thr Leu Leu Phe Thr Leu Ala Arg Pro Phe Thr Lys Ser

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atg caa cag gga gct gcc acc acc gtg tac tgt gct gct gtc cca gaa 1225

Met Gln Gln Gly Ala Ala Thr Thr Val Tyr Cys Ala Ala Val Pro Glu

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ctg gag ggt ctg gga ggg atg tac ttc aac aac tgc tgc cgc tgc atg 1273

Leu Glu Gly Leu Gly Gly Met Tyr Phe Asn Asn Cys Cys Arg Cys Met

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ccc tca cca gaa gct cag agc gaa gag acg gcc cgg acc ctg tgg gcg 1321

Pro Ser Pro Glu Ala Gln Ser Glu Glu Thr Ala Arg Thr Leu Trp Ala

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ctc agc gag agg ctg atc caa gaa cgg ctt ggc agc cag tcc ggc 1366

Leu Ser Glu Arg Leu Ile Gln Glu Arg Leu Gly Ser Gln Ser Gly

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<213> Homo sapiens

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Glu Leu Pro Pro Gly Trp Glu Glu Arg Thr Thr Lys Asp Gly Trp Val

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Tyr Tyr Ala Asn His Thr Glu Glu Lys Thr Gln Trp Glu His Pro Lys

35 40 45

Thr Gly Lys Arg Lys Arg Val Ala Gly Asp Leu Pro Tyr Gly Trp Glu

50 55 60

Gln Glu Thr Asp Glu Asn Gly Gln Val Phe Phe Val Asp His Ile Asn

65 70 75 80

Lys Arg Thr Thr Tyr Leu Asp Pro Arg Leu Ala Phe Thr Val Asp Asp

85 90 95

Asn Pro Thr Lys Pro Thr Thr Arg Gln Arg Tyr Asp Gly Ser Thr Thr

100 105 110

Ala Met Glu Ile Leu Gln Gly Pro Asp Phe Thr Gly Lys Val Val Val

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9/19

115

120

125

Val Thr Gly Ala Asn Ser Gly Ile Gly Phe Glu Thr Ala Lys Ser Phe

130

135

140

Ala Leu His Gly Ala His Val Ile Leu Ala Cys Arg Asn Met Ala Arg

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Ala Ser Glu Ala Val Ser Arg Ile Leu Glu Glu Trp His Lys Ala Lys

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Val Glu Ala Met Thr Leu Asp Leu Ala Leu Leu Arg Ser Val Gln His

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Phe Ala Glu Ala Phe Lys Ala Lys Asn Val Pro Leu His Val Leu Val

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Cys Asn Ala Ala Thr Phe Ala Leu Pro Trp Ser Leu Thr Lys Asp Gly

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Leu Glu Thr Thr Phe Gln Val Asn His Leu Gly His Phe Tyr Leu Val

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Gln Leu Leu Gln Asp Val Leu Cys Arg Ser Ala Pro Ala Arg Val Ile

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10/19

Val Val Ser Ser Glu Ser His Arg Phe Thr Asp Ile Asn Asp Ser Leu

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Gly Lys Leu Asp Phe Ser Arg Leu Ser Pro Thr Lys Asn Asp Tyr Trp

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Ala Met Leu Ala Tyr Asn Arg Ser Lys Leu Cys Asn Ile Leu Phe Ser

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Asn Glu Leu His Arg Arg Leu Ser Pro Arg Gly Val Thr Ser Asn Ala

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315

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Val His Pro Gly Asn Met Met Tyr Ser Asn Ile His Arg Ser Trp Trp

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Val Tyr Thr Leu Leu Phe Thr Leu Ala Arg Pro Phe Thr Lys Ser Met

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Gln Gln Gly Ala Ala Thr Thr Val Tyr Cys Ala Ala Val Pro Glu Leu

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Glu Gly Leu Gly Gly Met Tyr Phe Asn Asn Cys Cys Arg Cys Met Pro

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Ser Pro Glu Ala Gln Ser Glu Glu Thr Ala Arg Thr Leu Trp Ala Leu

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Ser Glu Arg Leu Ile Gln Glu Arg Leu Gly Ser Gln Ser Gly

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<213> Gallus gallus

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Val Ala Gly Gly Leu Pro Tyr Gly Trp Glu Gln Glu Thr Asp Glu Asn

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Gly Gln Val Tyr Phe Val Asp His Ile Asn Lys Arg Thr Thr Tyr Leu

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gat cca aga ttg gcc ttt aca gtt gaa gat aat cca gca aag cca cct 239

Asp Pro Arg Leu Ala Phe Thr Val Glu Asp Asn Pro Ala Lys Pro Pro

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act aga caa aaa

251

Thr Arg Gln Lys

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Glu Arg Thr Thr Lys Asp Gly Trp Val Tyr Tyr Ala Asn His Leu Glu

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Glu Lys Thr Gln Trp Glu His Pro Lys Ser Gly Lys Arg Lys Arg Val

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gga cag gtc tat ttt gta gac cac ata aac aaa aga act acc tat ctg 191

Ala Gly Gly Leu Pro Tyr Gly Trp Glu Gln Glu Thr Asp Glu Asn Gly

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Gln Val Tyr Phe Val Asp His Ile Asn Lys Arg Thr Thr Tyr Leu Asp

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Pro Arg Leu Ala Phe Thr Val Glu Asp Asn Pro Ala Lys Pro Pro Thr

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Arg Gln Lys

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<212> RNA

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Synthesized Sequence

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<211> 21

<212> DNA

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agcatcgcagt cggccttggtt g

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<210> 8

<211> 21

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